SEQUENCE LISTING

<110> ABURATANI, Hiroyuki
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TOKITA, Susumu

<120> ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE OF GPC3 PRESENT IN BLOOD

<140> PCT/JP03/11318
<141> 2003-09-04

<150> PCT/JP02/08999
<151> 2002-09-04

<160> 24

<170> PatentIn Ver. 2.1

<210> 1
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 1
gatatcatgg ccgggaccgt gcgcaccgcg t 31

<210> 2
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 2
gctagctcag tgcaccagga agaagaagca c 31

<210> 3
<211> 2300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (109)..(1851)

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gctccggctg ccactctccc gcgctctcct agctccctgc gaagcagg atg gcc ggg 117
Met Ala Gly
1
acc gtg cgc acc gcg tgc ttg gtg gtg gcg atg ctg ctc agc ttg gac 165
Thr Val Arg Thr Ala Cys Leu Val Val Ala Met Leu Leu Ser Leu Asp
5 10 15
ttc ccg gga cag gcg cag ccc ccg ccg ccg ccg ccg gac gcc acc tgt 213
Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp Ala Thr Cys
20 25 30 35

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cac caa gtc cgc tcc ttc ttc cag aga ctg cag ccc gga ctc aag tgg   261
His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu Lys Trp
                40                  45                  50
gtg cca gaa act ccc gtg cca gga tca gat ttg caa gta tgt ctc cct   309
Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys Leu Pro
            55                  60                  65
aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac caa cta   357
Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr Gln Leu
        70                  75                  80
aca gca cga ttg aac atg gaa cag ctg ctt cag tct gca agt atg gag   405
Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser Met Glu
    85                  90                  95
ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag gcc ttt   453
Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu Ala Phe
100                 105                 110                 115
gaa att gtt gtt cgc cat gcc aag aac tac acc aat gcc atg ttc aag   501
Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met Phe Lys
                120                 125                 130
aac aac tac cca agc ctg act cca caa gct ttt gag ttt gtg ggt gaa   549
Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val Gly Glu
            135                 140                 145
ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gac atc aat gta   597
Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile Asn Val
        150                 155                 160
gat gac atg gtc aat gaa ttg ttt gac agc ctg ttt cca gtc atc tat   645
Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val Ile Tyr
    165                 170                 175
acc cag cta atg aac cca ggc ctg cct gat tca gcc ttg gac atc aat   693
Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu Asp Ile Asn
180                 185                 190                 195
gag tgc ctc cga gga gca aga cgt gac ctg aaa gta ttt ggg aat ttc   741
Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly Asn Phe
                200                 205                 210
ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc act agg   789
Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val Thr Arg
            215                 220                 225
atc ttc ctt cag gct ctg aat ctt gga att gaa gtg atc aac aca act   837
Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn Thr Thr
        230                 235                 240
gat cac ctg aag ttc agt aag gac tgt ggc cga atg ctc acc aga atg   885
Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr Arg Met
    245                 250                 255
tgg tac tgc tct tac tgc cag gga ctg atg atg gtt aaa ccc tgt ggc   933
Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro Cys Gly
260                 265                 270                 275
ggt tac tgc aat gtg gtc atg caa ggc tgt atg gca ggt gtg gtg gag   981
Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val Val Glu
                280                 285                 290
att gac aag tac tgg aga gaa tac att ctg tcc ctt gaa gaa ctt gtg  1029
Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu Leu Val
            295                 300                 305
aat ggc atg tac aga atc tat gac atg gag aac gta ctg ctt ggt ctc  1077
Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu Gly Leu
        310                 315                 320
ttt tca aca atc cat gat tct atc cag tat gtc cag aag aat gca gga  1125
Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn Ala Gly
    325                 330                 335
aag ctg acc acc act att ggc aag tta tgt gcc cat tct caa caa cgc  1173
Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln Gln Arg
340                 345                 350                 355
caa tat aga tct gct tat tat cct gaa gat ctc ttt att gac aag aaa  1221
Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp Lys Lys
                360                 365                 370
gta tta aaa gtt gct cat gta gaa cat gaa gaa acc tta tcc agc cga  1269
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Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser Ser Arg
            375                 380                 385
aga agg gaa cta att cag aag ttg aag tct ttc atc agc ttc tat agt   1317
Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser Phe Tyr Ser
        390                 395                 400
gct ttg cct ggc tac atc tgc agc cat agc cct gtg gcg gaa aac gac   1365
Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala Glu Asn Asp
    405                 410                 415
acc ctt tgc tgg aat gga caa gaa ctc gtg gag aga tac agc caa aag   1413
Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr Ser Gln Lys
420                 425                 430                 435
gca gca agg aat gga atg aaa aac cag ttc aat ctc cat gag ctg aaa   1461
Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His Glu Leu Lys
                440                 445                 450
atg aag ggc cct gag cca gtg gtc agt caa att att gac aaa ctg aag   1509
Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp Lys Leu Lys
            455                 460                 465
cac att aac cag ctc ctg aga acc atg tct atg ccc aaa ggt aga gtt   1557
His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys Gly Arg Val
        470                 475                 480
ctg gat aaa aac ctg gat gag gaa ggg ttt gaa agt gga gac tgc ggt   1605
Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly Asp Cys Gly
    485                 490                 495
gat gat gaa gat gag tgc att gga ggc tct ggt gat gga atg ata aaa   1653
Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly Met Ile Lys
500                 505                 510                 515
gtg aag aat cag ctc cgc ttc ctt gca gaa ctg gcc tat gat ctg gat   1701
Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr Asp Leu Asp
                520                 525                 530
gtg gat gat gcg cct gga aac agt cag cag gca act ccg aag gac aac   1749
Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro Lys Asp Asn
            535                 540                 545
gag ata agc acc ttt cac aac ctc ggg aac gtt cat tcc ccg ctg aag   1797
Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser Pro Leu Lys
        550                 555                 560
ctt ctc acc agc atg gcc atc tcg gtg gtg tgc ttc ttc ttc ctg gtg   1845
Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe Phe Leu Val
    565                 570                 575
cac tga ctgcctggtg cccagcacat gtgctgccct acagcaccct gtggtcttcc    1901
His
580
tcgataaagg gaaccacttt cttatttttt tctatttttt ttttttgtt atcctgtata 1961
cctcctccag ccatgaagta gaggactaac catgtgttat gttttcgaaa atcaaatggt 2021
atcttttgga ggaagataca ttttagtggt agcatataga ttgtcctttt gcaaagaaag 2081
aaaaaaaacc atcaagttgt gccaaattat tctcctatgt ttggctgcta gaacatggtt 2141
accatgtctt tctctctcac tccctccctt tctatcgttc tctctttgca tggatttctt 2201
tgaaaaaaaa taaattgctc aaataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2261
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa                        2300

<210> 4
<211> 580
<212> PRT
<213> Homo sapiens

<400> 4
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Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro Pro Pro Asp
             20                  25                  30
Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly
         35                  40                  45
Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val
     50                  55                  60
Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys
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 65                  70                  75                  80
Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala
                85                  90                  95
Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln
            100                 105                 110
Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala
        115                 120                 125
Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe
    130                 135                 140
Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp
145                 150                 155                 160
Ile Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro
                165                 170                 175
Val Ile Tyr Thr Gln Leu Met Asn Pro Gly Leu Pro Asp Ser Ala Leu
            180                 185                 190
Asp Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe
        195                 200                 205
Gly Asn Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln
    210                 215                 220
Val Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile
225                 230                 235                 240
Asn Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu
                245                 250                 255
Thr Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys
            260                 265                 270
Pro Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly
        275                 280                 285
Val Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu
    290                 295                 300
Glu Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu
305                 310                 315                 320
Leu Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys
                325                 330                 335
Asn Ala Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser
            340                 345                 350
Gln Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile
        355                 360                 365
Asp Lys Lys Val Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu
    370                 375                 380
Ser Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Ser
385                 390                 395                 400
Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala
                405                 410                 415
Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val Glu Arg Tyr
            420                 425                 430
Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe Asn Leu His
        435                 440                 445
Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln Ile Ile Asp
    450                 455                 460
Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser Met Pro Lys
465                 470                 475                 480
Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe Glu Ser Gly
                485                 490                 495
Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser Gly Asp Gly
            500                 505                 510
Met Ile Lys Val Lys Asn Gln Leu Arg Phe Leu Ala Glu Leu Ala Tyr
        515                 520                 525
Asp Leu Asp Val Asp Asp Ala Pro Gly Asn Ser Gln Gln Ala Thr Pro
    530                 535                 540
Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn Val His Ser
545                 550                 555                 560
Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val Cys Phe Phe
                565                 570                 575
Phe Leu Val His
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<210> 5
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 5
atagaattcc accatggccg ggaccgtgcg c 31

<210> 6
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 6
ataggatccc ttcagcgggg aatgaacgtt c 31

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 7
gggccagtgg atagacagat g 21

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 8
gctcactgga tggtgggaag atg 23

<210> 9
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1389)

<220>
<223> Description of Artificial Sequence: Mouse-human
chimeric antibody (M3C11 H chain)

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atg aac ttc ggg ctc acc ttg att ttc ctt gtc ctt act tta aaa ggt 48
Met Asn Phe Gly Leu Thr Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
1 5 10 15
gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga ggc tta gtg aag 96

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Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30
cct gga gga tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc   144
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45
agt cgc tat gcc atg tct tgg gtt cgc cag att cca gag aag ata ctg   192
Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Ile Leu
    50                  55                  60
gag tgg gtc gca gcc att gat agt agt ggt ggt gac acc tac tat tta   240
Glu Trp Val Ala Ala Ile Asp Ser Ser Gly Gly Asp Thr Tyr Tyr Leu
65                  70                  75                  80
gac act gtg aag gac cga ttc acc atc tcc aga gac aat gcc aat aat   288
Asp Thr Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Asn
                85                  90                  95
acc ctg cac ctg caa atg cgc agt ctg agg tct gag gac aca gcc ttg   336
Thr Leu His Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Thr Ala Leu
            100                 105                 110
tat tac tgt gta aga cag ggg ggg gct tac tgg ggc caa ggg act ctg   384
Tyr Tyr Cys Val Arg Gln Gly Gly Ala Tyr Trp Gly Gln Gly Thr Leu
        115                 120                 125
gtc act gtc tct gca gct agc acc aag ggc cca tcg gtc ttc ccc ctg   432
Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    130                 135                 140
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc   480
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
145                 150                 155                 160
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca   528
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                165                 170                 175
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc   576
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
            180                 185                 190
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc   624
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
        195                 200                 205
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac   672
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
    210                 215                 220
acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac   720
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
225                 230                 235                 240
aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc   768
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
                245                 250                 255
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc   816
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270
cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag   864
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285
gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag   912
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc   960
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag   1008
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc   1056
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350
tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc   1104
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
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        355                 360                 365
cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg   1152
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat   1200
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400
ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc   1248
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg   1296
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430
tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg   1344
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga   1392
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460
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<210> 10
<211> 463
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M3C11 H chain)

<400> 10

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Met Asn Phe Gly Leu Thr Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
  1               5                  10                  15
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45
Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Ile Leu
    50                  55                  60
Glu Trp Val Ala Ala Ile Asp Ser Ser Gly Gly Asp Thr Tyr Tyr Leu
65                  70                  75                  80
Asp Thr Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Asn
                85                  90                  95
Thr Leu His Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Thr Ala Leu
            100                 105                 110
Tyr Tyr Cys Val Arg Gln Gly Gly Ala Tyr Trp Gly Gln Gly Thr Leu
        115                 120                 125
Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    130                 135                 140
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
145                 150                 155                 160
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                165                 170                 175
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
            180                 185                 190
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
        195                 200                 205
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
    210                 215                 220
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
225                 230                 235                 240
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
                245                 250                 255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
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        275                 280                 285
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460
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<210> 11
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1410)

<220>
<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M1E07 H chain)

<400> 11

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atg gga tgg aac tgg atc ttt att tta atc ctg tca gta act aca ggt   48
Met Gly Trp Asn Trp Ile Phe Ile Leu Ile Leu Ser Val Thr Thr Gly
  1               5                  10                  15
gtc cac tct gag gtc cag ctg cag cag tct gga cct gag ctg gtg aag   96
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
             20                  25                  30
cct ggg gct tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttc   144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
         35                  40                  45
act ggc tac tac atg cac tgg gtg aag caa agt cct gaa aag agc ctt   192
Thr Gly Tyr Tyr Met His Trp Val Lys Gln Ser Pro Glu Lys Ser Leu
     50                  55                  60
gag tgg att gga gag att aat cct agc act ggt ggt act acc tac aac   240
Glu Trp Ile Gly Glu Ile Asn Pro Ser Thr Gly Gly Thr Thr Tyr Asn
 65                  70                  75                  80
cag aag ttc aag gcc aag gcc aca ttg act gta gac aaa tcc tcc agc   288
Gln Lys Phe Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                 85                  90                  95
aca gcc tac atg cag ctc aag agc ctg aca tct gag gac tct gca gtc   336
Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
tat tac tgt gca agg agg ggc gga tta act ggg acg agc ttc ttt gct   384
Tyr Tyr Cys Ala Arg Arg Gly Gly Leu Thr Gly Thr Ser Phe Phe Ala
        115                 120                 125
tac tgg ggc caa ggg act ctg gtc act gtc tct gca gct agc acc aag   432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys
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    130                 135                 140
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg   480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg   528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc   576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg   624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac   672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc   720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa   768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac   816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac   864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc   912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac   960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg  1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca  1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa  1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac  1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc  1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc  1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag  1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc  1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc  1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
tcc ctg tct ccg ggt aaa tga                                     1413
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 12
<211> 470
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M1E07 H chain)

<400> 12

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Met Gly Trp Asn Trp Ile Phe Ile Leu Ile Leu Ser Val Thr Thr Gly
  1               5                  10                  15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45
Thr Gly Tyr Tyr Met His Trp Val Lys Gln Ser Pro Glu Lys Ser Leu
    50                  55                  60
Glu Trp Ile Gly Glu Ile Asn Pro Ser Thr Gly Gly Thr Thr Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Arg Gly Gly Leu Thr Gly Thr Ser Phe Phe Ala
        115                 120                 125
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
```

```
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470

<210> 13
<211> 1416
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1413)

<220>
<223> Description of Artificial Sequence: Mouse-human
      chimeric antibody (M19B11 H chain)

<400> 13
atg aac ttc ggg ctc acc ttg att ttc ctc gtc ctt act tta aaa ggt   48
Met Asn Phe Gly Leu Thr Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
  1               5                  10                  15
gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga gac tta gtg aag   96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
             20                  25                  30
cct gga ggg acc ctg aaa ctc tcc tgt gca gcc tct gga tcc act ttc   144
Pro Gly Gly Thr Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe
         35                  40                  45
agt aac tat gcc atg tct tgg gtt cgc cag act cca gag aag agg ctg   192
Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
     50                  55                  60
gag tgg gtc gca gcc att gat agt aat gga ggt acc acc tac tat cca   240
Glu Trp Val Ala Ala Ile Asp Ser Asn Gly Gly Thr Thr Tyr Tyr Pro
 65                  70                  75                  80
gac act atg aag gac cga ttc acc att tcc aga gac aat gcc aag aac   288
Asp Thr Met Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                 85                  90                  95
acc ctg tac ctg caa atg aac agt ctg agg tct gaa gac aca gcc ttt   336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Phe
            100                 105                 110
tat cac tgt aca aga cat aat gga ggg tat gaa aac tac ggc tgg ttt   384
Tyr His Cys Thr Arg His Asn Gly Gly Tyr Glu Asn Tyr Gly Trp Phe
        115                 120                 125
gct tac tgg ggc caa ggg act ctg gtc act gtc tct gca gct agc acc   432
Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
    130                 135                 140
aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct   480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160
ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa   528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175
ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac   576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190
acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc   624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc   672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag   720
```

```
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct   768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag   816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg   864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac   912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac   960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac  1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc  1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga  1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag  1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac  1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag  1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc  1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca  1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc  1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460
ctc tcc ctg tct ccg ggt aaa tga                                  1416
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 14
<211> 471
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M19B11 H chain)

<400> 14

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Met Asn Phe Gly Leu Thr Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
  1               5                  10                  15
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30
Pro Gly Gly Thr Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe
        35                  40                  45
Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
```

```
     50                  55                  60
Glu Trp Val Ala Ala Ile Asp Ser Asn Gly Gly Thr Thr Tyr Tyr Pro
 65                  70                  75                  80
Asp Thr Met Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Phe
            100                 105                 110
Tyr His Cys Thr Arg His Asn Gly Gly Tyr Glu Asn Tyr Gly Trp Phe
        115                 120                 125
Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
    130                 135                 140
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 15
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1410)

<220>

<223> Description of Artificial Sequence: Mouse-human
chimeric antibody (M18D04 H chain)

<400> 15

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atg gaa tct aac tgg ata ctt cct ttt att ctg tcg gta gct tca ggg   48
Met Glu Ser Asn Trp Ile Leu Pro Phe Ile Leu Ser Val Ala Ser Gly
  1               5                  10                  15
gtc tac tca gag gtt cag ctc cag cag tct ggg act gtg ctg gca agg   96
Val Tyr Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala Arg
             20                  25                  30
cct ggg gct tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt   144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
         35                  40                  45
act ggc tac tgg atg cgc tgg gta aaa cag agg cct gga cag ggt ctg   192
Thr Gly Tyr Trp Met Arg Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
     50                  55                  60
gaa tgg att ggc gct att tat cct gga aat agt gat aca aca tac aac   240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Thr Thr Tyr Asn
 65                  70                  75                  80
cag aag ttc aag ggc aag gcc aaa ctg act gca gtc aca tct gtc agc   288
Gln Lys Phe Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Val Ser
                 85                  90                  95
act gcc tac atg gaa ctc agc agc ctg aca aat gag gac tct gcg gtc   336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Asn Glu Asp Ser Ala Val
            100                 105                 110
tat tac tgt tca aga tcg ggg gac cta act ggg ggg ttt gct tac tgg   384
Tyr Tyr Cys Ser Arg Ser Gly Asp Leu Thr Gly Gly Phe Ala Tyr Trp
        115                 120                 125
ggc caa ggg act ctg gtc act gtc tct aca gcc aaa gct agc acc aag   432
Gly Gln Gly Thr Leu Val Thr Val Ser Thr Ala Lys Ala Ser Thr Lys
    130                 135                 140
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg   480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg   528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc   576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg   624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac   672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc   720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa   768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac   816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac   864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc   912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac   960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
```

```
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg   1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca   1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa   1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac   1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc   1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc   1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag   1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc   1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc   1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
tcc ctg tct ccg ggt aaa tga                                     1413
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 16
<211> 470
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M18D04 H chain)

<400> 16

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Met Glu Ser Asn Trp Ile Leu Pro Phe Ile Leu Ser Val Ala Ser Gly
  1               5                  10                  15
Val Tyr Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala Arg
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Gly Tyr Trp Met Arg Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Thr Thr Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Val Ser
                85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Asn Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ser Arg Ser Gly Asp Leu Thr Gly Gly Phe Ala Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Leu Val Thr Val Ser Thr Ala Lys Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
```

```
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 17
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(714)

<220>
<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M3C11 L chain)

<400> 17

```
atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa   48
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
  1               5                  10                  15
acc aac ggt gat gtt gtg atg acc cag act cca ctc act ttg tcg gtt   96
Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
             20                  25                  30
acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc   144
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
         35                  40                  45
tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca   192
Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
     50                  55                  60
ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ttg gac tct   240
```

```
Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
 65                  70                  75                  80
gga gcc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca   288
Gly Ala Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                 85                  90                  95
ctg aaa atc agt aga gtg gag gct gag gat ttg gga att tat tat tgc   336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
            100                 105                 110
tgg caa ggt aca cat ttt ccg ctc acg ttc ggt gct ggg acc aag ctg   384
Trp Gln Gly Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
        115                 120                 125
gag ctg aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca   432
Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140
tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg   480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160
aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac   528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175
gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc   576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            180                 185                 190
aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca   624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205
gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc   672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    210                 215                 220
ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga       717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 18
<211> 238
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M3C11 L chain)

<400> 18

```
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
  1               5                  10                  15
Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
             20                  25                  30
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
         35                  40                  45
Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
     50                  55                  60
Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
 65                  70                  75                  80
Gly Ala Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
                 85                  90                  95
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
            100                 105                 110
Trp Gln Gly Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
        115                 120                 125
Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175
```

```
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            180                 185                 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    210                 215                 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 19
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(714)

<220>
<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M1E07 L chain)

<400> 19

```
atg agt cct gtc cag ttc ctg ttt ctg tta atg ctc tgg att cag gaa   48
Met Ser Pro Val Gln Phe Leu Phe Leu Leu Met Leu Trp Ile Gln Glu
  1               5                  10                  15
acc aac ggt gat gtt gtg atg acc cag act cca ctg tct ttg tcg gtt   96
Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val
             20                  25                  30
acc att gga caa cca gcc tct atc tct tgc aag tca agt cag agc ctc   144
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
         35                  40                  45
tta tat agt aat gga aag aca tat ttg aat tgg tta caa cag agg cct   192
Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro
     50                  55                  60
ggc cag gct cca aag cac cta atg tat cag gtg tcc aaa ctg gac cct   240
Gly Gln Ala Pro Lys His Leu Met Tyr Gln Val Ser Lys Leu Asp Pro
 65                  70                  75                  80
ggc atc cct gac agg ttc agt ggc agt gga tca gaa aca gat ttt aca   288
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr
                 85                  90                  95
ctt aaa atc agc aga gtg gag gct gaa gat ttg gga gtt tat tac tgc   336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110
ttg caa agt aca tat tat ccg ctc acg ttc ggt gct ggg acc aag ctg   384
Leu Gln Ser Thr Tyr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
        115                 120                 125
gag ctg aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca   432
Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140
tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg   480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160
aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac   528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175
gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc   576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            180                 185                 190
aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca   624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205
gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc   672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
```

```
    210                 215                 220
ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga       717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235

<210> 20
<211> 238
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human
      chimeric antibody (M1E07 L chain)

<400> 20
Met Ser Pro Val Gln Phe Leu Phe Leu Leu Met Leu Trp Ile Gln Glu
  1               5                  10                  15
Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val
            20                  25                  30
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
        35                  40                  45
Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro
    50                  55                  60
Gly Gln Ala Pro Lys His Leu Met Tyr Gln Val Ser Lys Leu Asp Pro
65                  70                  75                  80
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr
                85                  90                  95
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
            100                 105                 110
Leu Gln Ser Thr Tyr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
        115                 120                 125
Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            180                 185                 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    210                 215                 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235

<210> 21
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(702)

<220>
<223> Description of Artificial Sequence: Mouse-human
      chimeric antibody (M19B11 L chain)

<400> 21
atg aga ccc tcc att cag ttc ctg ggg ctc ttg ttg ttc tgg ctt cat   48
Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
  1               5                  10                  15
ggt gtt cag tgt gac atc cag atg aca cag tct cca tcc tca ctg tct   96
Gly Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
```

```
             20                  25                  30
gca tct ctg gga ggc aaa gtc acc atc act tgc aag gca agt cag gac   144
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
         35                  40                  45
att aac aag aat ata gtt tgg tac caa cac aag cct gga aaa ggt cct   192
Ile Asn Lys Asn Ile Val Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
     50                  55                  60
agg ctg ctc ata tgg tac aca tct aca tta cag cca ggc atc cca tca   240
Arg Leu Leu Ile Trp Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
 65                  70                  75                  80
agg ttc agt gga agt ggg tct ggg aga gat tat tcc ttc agc atc agc   288
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
                 85                  90                  95
aac ctg gag cct gaa gat att gca act tat tac tgt cta cag tat gat   336
Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
            100                 105                 110
aat ctt cca cgg acg ttc ggt gga ggc acc aaa ctg gaa atc aaa cgt   384
Asn Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125
acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag   432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140
ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat   480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg   528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc   576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa   624
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc   672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220
gtc aca aag agc ttc aac agg gga gag tgt tga                       705
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 22
<211> 234
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M19B11 L chain)

<400> 22

```
Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
  1               5                  10                  15
Gly Val Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
             20                  25                  30
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
         35                  40                  45
Ile Asn Lys Asn Ile Val Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
     50                  55                  60
Arg Leu Leu Ile Trp Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
 65                  70                  75                  80
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
                 85                  90                  95
Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
            100                 105                 110
```

```
Asn Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230

<210> 23
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(717)

<220>
<223> Description of Artificial Sequence: Mouse-human
      chimeric antibody (M18D04 L chain)

<400> 23
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct   48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
  1               5                  10                  15
gga tcc act gca gat att gtg atg acg cag gct gca ttc tcc aat cca   96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
             20                  25                  30
gtc act ctt gga aca tca act tcc atc tcc tgc agg tct agt aag agt   144
Val Thr Leu Gly Thr Ser Thr Ser Ile Ser Cys Arg Ser Ser Lys Ser
         35                  40                  45
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag   192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
     50                  55                  60
cca ggc cag tct cct cag ctc ctg att tat cag atg tcc aac ctt gcc   240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65                  70                  75                  80
tca gga gtc cca gac agg ttc agt agc agt ggg tca gga act gat ttc   288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                 85                  90                  95
aca ctg aga atc agc aga gtg gag gct gag gat gtg ggt gtt tat tac   336
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110
tgt gct caa aat cta gaa ctt ccg tat acg ttc gga tcg ggg acc aag   384
Cys Ala Gln Asn Leu Glu Leu Pro Tyr Thr Phe Gly Ser Gly Thr Lys
        115                 120                 125
ctg gaa ata aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg   432
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg   480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat   528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175
```

```
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac   576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa   624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag   672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga   720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 24
<211> 239
<212> PRT
<213> Artificial Sequence

<223> Description of Artificial Sequence: Mouse-human chimeric antibody (M18D04 L chain)

<400> 24

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
  1               5                  10                  15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
            20                  25                  30
Val Thr Leu Gly Thr Ser Thr Ser Ile Ser Cys Arg Ser Ser Lys Ser
        35                  40                  45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    50                  55                  60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65                  70                  75                  80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110
Cys Ala Gln Asn Leu Glu Leu Pro Tyr Thr Phe Gly Ser Gly Thr Lys
        115                 120                 125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```